

Nucleotide sequence of the tamarillo mosaic virus coat protein gene

Robin M.Eagles^{1, 2}, Richard C.Gardner² and Richard L.S.Forster¹

¹DSIR Plant Protection, Private Bag, Auckland and ²Department of Cellular and Molecular Biology, University of Auckland, Auckland, New Zealand

Submitted October 25, 1990

EMBL accession no. X54804

Tamarillo mosaic virus (TaMV), a member of the potyvirus group, causes yield loss and fruit blemishing in tamarillo (*Cyphomandra betacea* Sendt.) (1). Potyvirus genomes contain approximately 10 kb of a single stranded RNA and are translated as a polyprotein that is subsequently proteolytically cleaved.

A cDNA clone covering the 3' terminus of TaMV (strain R) has been isolated and sequenced; part of this sequence is shown in the figure below. N-terminal sequencing of the first 10 amino acids of purified virus coat protein identified the beginning of the coat protein gene in the cDNA sequence (sequenced amino acids are underlined). The amino acid residues immediately upstream of the coat protein gene are homologous to proteolytic cleavage sites preceding the coat protein genes of other potyviruses (2, 3). T₇ RNA transcripts were synthesized from a cDNA clone containing an in-frame AUG initiation codon immediately 5' of the coat protein gene. An *in vitro* translation product synthesized from this RNA comigrated with the native coat protein and was immunoprecipitated by antibodies raised against purified virus (data not shown).

The TaMV coat protein shows 55–66% amino acid identity to the coat proteins of eleven distinct members of the potyvirus

group. This level of homology suggests that TaMV is an independent member of the potyvirus group rather than a strain of an existing member (4). The TaMV 3' untranslated sequence shows less than 50% homology with other potyviruses, providing further support for this conclusion (5).

ACKNOWLEDGEMENTS

This work was supported by the Agricultural Marketing Research and Development Trust and the New Zealand Tamarillo Growers' Association.

REFERENCES

1. Mossop,D.W. (1977) *N.Z. J. Agr. Res.* **20**, 535–541.
2. Dougherty,W.G., Cary,S.M. and Parks,T.D. (1989) *Virology* **171**, 356–364.
3. Domier,L.L., Franklin,K.M., Shahabuddin,M., Hellmann,G.M., Overmeyer,J.H., Hiremath,S.T., Siaw,M.F.E., Lomonosoff,G.P., Shaw,J.G. and Rhoads,R.E. (1986) *Nucl. Acids Res.* **14**, 5417–5430.
4. Shukla,D. and Ward,C.W. (1989) *Adv. Virus Res.* **36**, 273–314.
5. Frenkel,M.J., Ward,C.W. and Shukla,D.D. (1989) *J. Gen. Virol.* **70**, 2775–2783.

1	GTAGATGAAGAGGATGACATAGTCTATTCCAGGCTGGAAACCTTGATGCAGGTGAACCGACAGCACAAAAGCAGAGGGAAAGAAGAAGGAAGGAGAGG	100
V D E E D D I V Y F Q A G T L D A G E A T A Q K A E G K K K E G E V		
101 TTTCAAGCGGAAAGCCCTCGTTGTAAGATAAGGATGTCGATTAGGTACTGCTGGGACACATTCAAGTACACGCTTAAAGTCATGACATCAAAGCT	200	
S S G K A V V V K D D L G T A G T H S V P R L K S M T S K L		
201 CACACTGCCAATGCTCAAAGGTAAGTCGTTGTAACTTAGATCACTTGCTATCCCTATAAACAAACAGTCGATTATCAAATGCTAGAGCCACCCACGAA	300	
T L P M L K G K S R C N L D H L L S Y K Q T V D L S N A R A T H E		
301 CAATTCAAATTGGTATGATGGTGTGATGGCTAGTTATGAGCTGGAAAGATCAAGCATGGAAATCATCCTCAATGGTTTATGGTATGGTCATTGAAA	400	
Q F Q N W Y D G V M A S Y E L E E S S M E I I L N G F M V W C I E N		
401 ATGGGACATCTCCTGACATAATGGAGTCTGGACCATGATGGACGATGAAGAACAGATATCGTACCCACTAAACCCATGCTTATGCAAGCCTTC	500	
G T S P D I N G V W T M M D D E E E Q I S Y P L K P M L D H A K P S		
501 TTTAAGGCAAATAATGAGGCATTTCAGTGCCTCGCAGAGGCGTATATTGAGATGAGAAGTCGTGAGAACGCCATACATGCCCAAGGTATGGTTACAACGC	600	
L R Q I M R H F S A L A E A Y I E M R S R E K P Y M P R Y G L Q R		
601 AATTGAGAGATCAAAGTTGGCAAGGTATGCATTGATTTCTATGAGATCACTGCAACCCTCGGTCAAGGCCAAGGAGGCATTTGCAAATGAAGG	700	
N L R D Q S L A R Y A F D F Y E I T A T T P V R A K E A H L Q M K A		
701 CAGCTGGCTGAAGAATTGCAACACTAACATGTTGGACTGGACGGAAATGTCACAACCTCGGAAGAGGACACAGAAAGGCACACAGCAACGGATGTTAA	800	
A A L K N S N T N M F G L D G N V T T S E E D T E R H T A T D V N		
801 TCGCAACATGCACTCCTCTGGCGTGAAGGGGTGTAACCGAAAGTGCCGTACTATTATATAAGAGTCCCTGTTAGTATCCTTGCTTATTATT	900	
R N M H H L L G V K G V		
901 AGAATACGTTATCTTCAACAAGTATGATATTGCTCTCACCTCGCAATAGTGAGTTGAGTGGAAATAAGTACTAGTATTCTATGGCCTACTTG	1000	
1001 TTATATAGACCCACACCTAGTGAGATTATCTCGTGAATGGTTTATGTTCAACTGTCAGGG (A) 27	1066	